

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 4.11802 Seconds
(without alignments)
1690.542 Million cell updates/sec

Title: US-10-624-932-2_COPY_372_389

Perfect score: 86

Sequence: 1 LVLLLLVLILVYCRKKEG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	86	100.0	130	4	AAM25451	Aam25451 Human pro
2	86	100.0	266	4	AAB50650	Aab50650 Human UNC
3	86	100.0	335	8	ADH71616	Adh71616 Human pro
4	86	100.0	544	7	ADG42581	Adg42581 Human tra
5	86	100.0	556	2	AAW78899	Aaw78899 Human UNC
6	86	100.0	817	8	ADH71624	Adh71624 Human pro
7	86	100.0	833	8	ADH71622	Adh71622 Human pro
8	86	100.0	842	5	AAU74818	Aau74818 Human REP
9	86	100.0	842	8	ADL06574	Adl06574 Human tum

10	86	100.0	898	5	AAU85403	Aau85403	Human pro
11	86	100.0	898	5	AAU97899	Aau97899	Human net
12	86	100.0	898	8	ADH71618	Adh71618	Human pro
13	86	100.0	898	8	ADH71626	Adh71626	Human pro
14	86	100.0	899	5	AAU79939	Aau79939	Human UNC
15	86	100.0	899	7	ADG42569	Adg42569	Novel hum
16	86	100.0	899	8	ADH71636	Adh71636	Human pro
17	86	100.0	899	8	ADH71642	Adh71642	Human pro
18	86	100.0	899	8	ADH71648	Adh71648	Human pro
19	86	100.0	899	8	ADH71632	Adh71632	Human pro
20	86	100.0	899	8	ADH71610	Adh71610	Human pro
21	86	100.0	899	8	ADH71628	Adh71628	Human pro
22	86	100.0	899	8	ADH71640	Adh71640	Human pro
23	86	100.0	899	8	ADH71650	Adh71650	Human pro
24	86	100.0	899	8	ADH71644	Adh71644	Human pro
25	86	100.0	899	8	ADH71634	Adh71634	Human pro
26	86	100.0	899	8	ADH71646	Adh71646	Human pro
27	86	100.0	899	8	ADH71638	Adh71638	Human pro
28	86	100.0	943	4	AAM79128	Aam79128	Human pro
29	79	91.9	899	8	ADH71630	Adh71630	Human pro
30	68	79.1	898	2	AAW78898	Aaw78898	Rat UNC-5
31	68	79.1	898	5	AAU10543	Aau10543	Rat netri
32	68	79.1	898	5	AAU97900	Aau97900	Rat netri
33	68	79.1	898	7	ADG42580	Adg42580	Rat trans
34	58	67.4	754	3	AAG39446	Aag39446	Arabidops
35	58	67.4	978	3	AAG39445	Aag39445	Arabidops
36	58	67.4	1173	3	AAG39444	Aag39444	Arabidops
37	58	67.4	1173	4	AAB37602	Aab37602	FLR1 rece
38	56	65.1	245	2	AAW98409	Aaw98409	H. pylori
39	53	61.6	826	3	AAY96513	Aay96513	Human Zsi
40	53	61.6	826	8	ADS17119	Ads17119	Human mem
41	53	61.6	837	4	ABG19458	Abg19458	Novel hum
42	52	60.5	408	2	AAW75856	Aaw75856	Human sec
43	52	60.5	408	2	AAY45161	Aay45161	Human sec
44	52	60.5	892	7	ADJ68848	Adj68848	Human hea
45	48	55.8	595	4	ABB11999	Abb11999	Human Lut

ALIGNMENTS

RESULT 1

AAM25451

ID AAM25451 standard; protein; 130 AA.

XX

AC AAM25451;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:966.

XX

KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregate; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.

XX

OS Homo sapiens.

XX

PN WO200153455-A2.

XX

PD 26-JUL-2001.

XX

PF 22-DEC-2000; 2000WO-US035017.

XX

PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457603/49.
DR N-PSDB; AAH99392.

XX

PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX

PS Claim 20; Page 204; 1217pp; English.

XX

CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders

XX

SQ Sequence 130 AA;

Query Match 100.0%; Score 86; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 42 LVLLLLVLILVYCRKKEG 59

RESULT 2

AAB50650

ID AAB50650 standard; protein; 266 AA.

XX

AC AAB50650;

XX

DT 19-MAR-2001 (first entry)

XX

DE Human UNC-5H1 protein translation in frame 2 sequence SEQ ID NO:9.

XX

KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
protein-protein interaction; identification.

XX

OS Homo sapiens.

XX

PN WO200073328-A2.

XX

PD 07-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-EP005108.

XX

PR 01-JUN-1999; 99GB-00012755.

XX

PA (DEVG-) DEVGEM NV.

XX

PI Van Crielinge W, Roelens I, Bogaert T, Verwaerde P;

XX

DR WPI; 2001-016508/02.

XX

PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
PT identifying unknown human cDNAs which encode proteins that interact with
PT the human unc-5C protein.

XX

PS Disclosure; Page 106-107; 246pp; English.

XX

CC The present invention describes 3 variants of human unc-5C cDNAs (unc-
CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
CC protein-protein-interactions between the unc-5 protein and a variety of
CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
CC cDNA are useful in methods for identifying compounds which reduce or
CC inhibit the lethal phenotype associated with the expression of the unc-5
CC death domain in yeast. They are also useful in yeast two hybrid
CC experiments for identifying unknown human cDNAs which encode proteins
CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and

CC AAB50646 to AAB50693 represent sequences used in the exemplification of
CC the present invention

XX

SQ Sequence 266 AA;

Query Match 100.0%; Score 86; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 27 LVLLLLVLILVYCRKKEG 44

RESULT 3

ADH71616

ID ADH71616 standard; protein; 335 AA.

XX

AC ADH71616;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21d SEQ ID NO:512.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR N-PSDB; ADH71615.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 512; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.
XX
SQ Sequence 335 AA;

Query Match 100.0%; Score 86; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 291 LVLLLLVLILVYCRKKEG 308

RESULT 4
ADG42581
ID ADG42581 standard; protein; 544 AA.
XX
AC ADG42581;
XX
DT 26-FEB-2004 (first entry)
XX

DE Human transmembrane receptor Unc5H1 homologue.
XX
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; human; transmembrane receptor;
KW Unc5H1 homologue.
XX
OS Homo sapiens.
XX
PN US2003204052-A1.
XX
PD 30-OCT-2003.
XX
PF 04-OCT-2001; 2001US-00970944.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2003-900673/82.
XX
PT New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.
XX
PS Disclosure; SEQ ID NO 14; 118pp; English.
XX
CC The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residues
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
CC the amino acid sequence of a transmembrane receptor homologue used in a
CC comparison with the novel human proteins of the invention.
XX
SQ Sequence 544 AA;

Query Match 100.0%; Score 86; DB 7; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
Db 18 LVLLLLVLILVYCRKKEG 35

RESULT 5
AAW78899
ID AAW78899 standard; protein; 556 AA.
XX
AC AAW78899;

XX
DT 25-MAR-2003 (revised)
DT 21-DEC-1998 (first entry)
XX
DE Human UNC-5 homologue UNC5H-1.
XX
KW UNC-5; UNC5H-1; human; netrin receptor; cell migration; axon guidance;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT /note= "encoded by TG"
FT Misc-difference 67
FT /note= "encoded by ATCT"
FT Misc-difference 256
FT /note= "encoded by GC"
FT Misc-difference 262
FT /note= "encoded by TG"
FT Misc-difference 360
FT /note= "encoded by AG"
FT Misc-difference 367
FT /note= "encoded by CC"
FT Misc-difference 370
FT /note= "encoded by TC"
FT Misc-difference 542
FT /note= "encoded by GG"
XX
PN WO9837085-A1.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US003143.
XX
PR 19-FEB-1997; 97US-00808982.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
XX
DR WPI; 1998-495364/42.
DR N-PSDB; AAW78899.
XX
PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
PT the biopharmaceutical industry.
XX
PS Claim 1; Page 22-23; 32pp; English.
XX
CC UNC5H-1 and UNC5H-2 (see AAW78901) are human homologues of *Caenorhabditis*
CC elegans UNC-5 protein. Their amino acid sequences were deduced from
CC isolated unc5h cDNA clones (see AAV52941 and AAV52943) isolated from an
CC embryonic brain cDNA library. The predicted proteins show similarity with
CC UNC-5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin
CC type-1 repeats, a predicted membrane spanning region, and a large
CC intracellular domain. They are predicted to be involved in cell migration
CC and axon guidance, and are characterised as receptor proteins for

CC netrins. Rat UNC5H-1 (see AAW78898) and UNC5H-2 (see AAW78900) proteins
CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly
CC from transfected host cells. The invention also provides unc-5
CC hybridisation probes and primers, vertebrate UNC-5-specific binding
CC agents such as specific antibodies, and methods of making and using the
CC subject compositions in diagnosis (e.g. genetic hybridisation screens for
CC vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate
CC vertebrate unc-5 gene expression) and in the biopharmaceutical industry
CC (e.g. as immunogens, reagents for modulating cell guidance, reagents for
CC screening chemical libraries for lead pharmacological agents, etc.).
CC (Updated on 25-MAR-2003 to correct PI field.)

xx

SQ Sequence 556 AA;

```

Query Match          100.0%;  Score 86;  DB 2;  Length 556;
Best Local Similarity 100.0%;  Pred. No. 0.0008;
Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Y      1 LVLLLLVLILVYCRKKEG 18
       ||||||| | | | | | |
D      30 LVLLLLVLILVYCRKKEG 47

```

RESULT 6

ADH71624

ID ADH71624 standard; protein; 817 AA.

xx

AC ADH71624;

xx

DT 25-MAR-2004 (first entry)

八

DE human protein of the invention NOV2011 SEQ ID NO:320.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

xx

OS *Homo sapiens.*

xx

PN WO2003102155-A2.

三

FD 11-DEC-2003.
VV

xx

11 08 JAN 2008, 2008WS 0501,1500
XX

PR

PR 04-JUN-2002: 2002US-0385784P-

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71623.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 520; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 817 AA;

Query Match 100.0%; Score 86; DB 8; Length 817;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18

|||||||||||||||||||

Db 291 LVLLLLVLILVYCRKKEG 308

RESULT 7
ADH71622
ID ADH71622 standard; protein; 833 AA.
XX
AC ADH71622;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV21g SEQ ID NO:518.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71621.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 518; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 833 AA;

Query Match 100.0%; Score 86; DB 8; Length 833;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | |
Db 307 LVLLLLVLILVYCRKKEG 324

RESULT 8

AAU74818

ID AAU74818 standard; protein; 842 AA.

XX

AC AAU74818;

XX

DT 23-APR-2002 (first entry)

XX

DE Human REPTR 1 protein.

XX

KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;
KW anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective;
KW antiallergic; antibody; immunogen; endometriosis;
KW gastrointestinal disorder; gastritis; oesophageal carcinoma;
KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;
KW endocrine disorder; hypothalamus disorder; Kallman's disease;
KW autoimmune disease; inflammatory disease; infertility; receptor;
KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;
KW osteoarthritis; diabetes mellitus; multiple sclerosis;
KW systemic lupus erythematosus; cell proliferative disorder; cancer;
KW developmental disorder; Duchenne muscular dystrophy;

KW Becker muscular dystrophy; neurological disorder; epilepsy;
KW Alzheimer's disease; Huntington's disease; reproductive disorder.
XX
OS Homo sapiens.
XX
PN WO200198354-A2.
XX
PD 27-DEC-2001.
XX
PF 21-JUN-2001; 2001WO-US019942.
XX
PR 21-JUN-2000; 2000US-0214027P.
PR 25-AUG-2000; 2000US-0228045P.
PR 12-DEC-2000; 2000US-0255104P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;
PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;
XX
DR WPI; 2002-090432/12.
DR N-PSDB; ABK15169.
XX
PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
PT the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
PT proliferative (e.g. cancer)disorders.
XX
PS Claim 45; Page 111-113; 157pp; English.
XX
CC This invention relates to twelve human receptors cDNA sequences referred
CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The
CC proteins of the invention may have antiinflammatory, cytostatic,
CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
CC general, anticonvulsant, nootropic, neuroprotective, antiallergic
CC activities. The sequences of the invention may be used to produce REPTR
CC agonists or antagonists, and the protein sequences may be used to raise
CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and
CC polypeptides of the invention are useful in the diagnosis,treatment and
CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,
CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine
CC (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory
CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,
CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,
CC systemic lupus erythematosus), cell proliferative (e.g. cancer),
CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological
CC (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and
CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other
CC examples of each disorder are given in the specification. The present
CC sequence represents the human REPTR1 protein sequence of the invention
XX
SQ Sequence 842 AA;

Query Match 100.0%; Score 86; DB 5; Length 842;
Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | |
Db 316 LVLLLLVLILVYCRKKEG 333

RESULT 9
ADL06574
ID ADL06574 standard; protein; 842 AA.
XX
AC ADL06574;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) polypeptide #73.
XX
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
PA (GETH) GENENTECH INC.
XX
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
XX
DR WPI; 2004-257144/24.
DR N-PSDB; ADL06497.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
XX
PS Claim 2; SEQ ID NO 154; 319pp; English.
XX
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence

CC represents a human TAT polypeptide of the invention.

XX

SQ Sequence 842 AA;

Query Match 100.0%; Score 86; DB 8; Length 842;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 316 LVLLLLVLILVYCRKKEG 333

RESULT 10

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.

PR 15-AUG-2000; 2000US-0225470P.

PR 16-AUG-2000; 2000US-0225697P.

PR 01-FEB-2001; 2001US-0263662P.

PR 05-APR-2001; 2001US-0281645P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
DR WPI; 2002-180074/23.
DR N-PSDB; ABK37922.
XX
PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
PS Claim 1; Page 11; 213pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence represents a
CC NOVX protein
XX
SQ Sequence 898 AA;

Query Match 100.0%; Score 86; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 372 LVLLLLVLILVYCRKKEG 389

RESULT 11
AAU97899
ID AAU97899 standard; protein; 898 AA.
XX
AC AAU97899;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human netrin binding membrane receptor UNC5H-1 protein.

XX
KW Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic;
KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
KW central nervous system; CNS; stroke; Parkinson's disease;
KW multiple sclerosis; Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 152. .223
FT /note= "Immunoglobulin domain "
FT Domain 247. .294
FT /note= "Thrombospondine type 1 domain "
FT Domain 302. .348
FT /note= "Thrombospondine type 1 domain"
FT Region 361. .382
FT /note= "Transmembrane region"
FT Domain 495. .598
FT /note= "ZU5 domain"
FT Domain 817. .897
FT /note= "Death domain"
XX
PN WO200233080-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-EP011891.
XX
PR 16-OCT-2000; 2000US-0240061P.
XX
PA (FARB) BAYER AG.
XX
PI Koehler RH;
XX
DR WPI; 2002-463314/49.
DR N-PSDB; ABK52891.
XX
PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX
PS Claim 1; Fig 2; 94pp; English.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g., Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating

PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002, 200203-0
XX
PA (CURA-) CURAGEN CORP.

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX
DR WPI; 2004-081935/08.
DP N-PSDB: ADH71617

XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX
PS Example 21; SEQ ID NO 514; 1880pp; English.

XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

SO Sequence 898 AA;

Query Match 100.0%; Score 86; DB 8; Length 898;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
ADH71626
ID ADH71626 standard; protein; 898 AA.
XX
AC ADH71626;

XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV21i SEQ ID NO:522.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71625.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX
PS Example 21; SEQ ID NO 522; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX
SQ Sequence 898 AA;

Query Match 100.0%; Score 86; DB 8; Length 898;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | |
Db 372 LVLLLLVLILVYCRKKEG 389

RESULT 14
AAU79939
ID AAU79939 standard; protein; 899 AA.
XX
AC AAU79939;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human UNC5-like protein NOV1.
XX
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13.
XX
OS Homo sapiens.
XX
PN WO200229038-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031377.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (CURA-) CURAGEN CORP.
XX

PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2002-340104/37.
DR N-PSDB; ABK49422.
XX
PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, atherosclerosis, and cancer.
XX
PS Claim 1; Page 9; 180pp; English.
XX
CC The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present amino acid sequence is that of the human UNC5-like
CC protein NOV1 of the invention. This sequence is encoded by the human UNC5
CC -like NOV1 gene located on chromosome 13
XX
SQ Sequence 899 AA;

Query Match 100.0%; Score 86; DB 5; Length 899;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 373 LVLLLLVLILVYCRKKEG 390

RESULT 15
ADG42569
ID ADG42569 standard; protein; 899 AA.
XX
AC ADG42569;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human NOV1.
XX
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; human.
XX
OS Homo sapiens.
XX
PN US2003204052-A1.
XX
PD 30-OCT-2003.
XX
PF 04-OCT-2001; 2001US-00970944.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX

PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2003-900673/82.
DR N-PSDB; ADG42568.
XX
PT New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.
XX
PS Claim 1; SEQ ID NO 2; 118pp; English.
XX
CC The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residues
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
CC the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 899 AA;

Query Match 100.0%; Score 86; DB 7; Length 899;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 LVLLLLVLILVYCRKKEG 18
Db 373 LVLLLLVLILVYCRKKEG 390

Search completed: March 1, 2005, 08:56:48
Job time : 5.11802 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:42:47 ; Search time 1.07853 Seconds
(without alignments)
1245.848 Million cell updates/sec

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Perfect score: 86

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Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	86	100.0	557	3	US-09-306-902A-6	Sequence 6, Appli
3	68	79.1	898	2	US-08-808-982-5	Sequence 5, Appli
4	68	79.1	898	3	US-09-306-902A-5	Sequence 5, Appli
5	52	60.5	408	2	US-09-014-969-13	Sequence 13, Appli
6	48	55.8	66	4	US-09-248-796A-23224	Sequence 23224, A
7	47	54.7	91	4	US-09-198-452A-1162	Sequence 1162, Ap
8	47	54.7	109	4	US-09-438-185A-175	Sequence 175, App
9	46	53.5	387	1	US-08-123-161A-10	Sequence 10, Appli
10	46	53.5	387	1	US-08-123-161A-12	Sequence 12, Appli
11	46	53.5	387	1	US-08-483-278-10	Sequence 10, Appli

12	46	53.5	387	1	US-08-483-278-12	Sequence 12, Appl
13	46	53.5	392	4	US-09-949-016-9728	Sequence 9728, Ap
14	45	52.3	483	4	US-09-489-039A-10360	Sequence 10360, A
15	45	52.3	635	4	US-10-101-464A-932	Sequence 932, App
16	44	51.2	238	4	US-09-270-767-33105	Sequence 33105, A
17	44	51.2	238	4	US-09-270-767-48322	Sequence 48322, A
18	44	51.2	255	4	US-09-198-452A-123	Sequence 123, App
19	44	51.2	285	4	US-09-438-185A-107	Sequence 107, App
20	44	51.2	303	4	US-09-651-200-23	Sequence 23, Appl
21	44	51.2	303	4	US-09-441-411-15	Sequence 15, Appl
22	44	51.2	303	4	US-09-441-411-20	Sequence 20, Appl
23	44	51.2	309	2	US-08-456-104-4	Sequence 4, Appli
24	44	51.2	309	3	US-08-479-744A-23	Sequence 23, Appl
25	44	51.2	309	3	US-08-280-757B-23	Sequence 23, Appl
26	44	51.2	309	3	US-08-205-697A-21	Sequence 21, Appl
27	44	51.2	309	3	US-08-702-525-21	Sequence 21, Appl
28	44	51.2	309	4	US-09-651-200-22	Sequence 22, Appl
29	44	51.2	309	4	US-09-667-135-33	Sequence 33, Appl
30	44	51.2	309	4	US-09-425-762-23	Sequence 23, Appl
31	44	51.2	309	4	US-09-837-867A-21	Sequence 21, Appl
32	44	51.2	309	4	US-09-206-132-4	Sequence 4, Appli
33	44	51.2	309	4	US-09-441-411-13	Sequence 13, Appl
34	44	51.2	309	4	US-09-441-411-18	Sequence 18, Appl
35	44	51.2	309	4	US-09-441-411-24	Sequence 24, Appl
36	44	51.2	309	4	US-09-425-516-23	Sequence 23, Appl
37	44	51.2	309	5	PCT-US95-02576-21	Sequence 21, Appl
38	44	51.2	314	3	US-08-205-697A-13	Sequence 13, Appl
39	44	51.2	314	3	US-08-702-525-13	Sequence 13, Appl
40	44	51.2	314	4	US-09-837-867A-13	Sequence 13, Appl
41	44	51.2	314	4	US-09-441-411-14	Sequence 14, Appl
42	44	51.2	314	4	US-09-441-411-19	Sequence 19, Appl
43	44	51.2	314	5	PCT-US95-02576-13	Sequence 13, Appl
44	44	51.2	356	4	US-09-441-411-11	Sequence 11, Appl
45	44	51.2	356	4	US-09-441-411-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
 US-08-808-982-6
; Sequence 6, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA

; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-6

Query Match 100.0%; Score 86; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
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Db 30 LVLLLLVLILVYCRKKEG 47

RESULT 2
US-09-306-902A-6
; Sequence 6, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-306-902A-6

Query Match 100.0%; Score 86; DB 3; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
||| ||| ||| ||| |||
Db 30 LVLLLLVLILVYCRKKEG 47

RESULT 3

US-08-808-982-5

; Sequence 5, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide

US-08-808-982-5

Query Match 79.1%; Score 68; DB 2; Length 898;
Best Local Similarity 77.8%; Pred. No. 0.05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| |||| | |:|||||||
Db 372 LFLLLLALGLIYCRKKEG 389

RESULT 4

US-09-306-902A-5

; Sequence 5, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-306-902A-5

Query Match 79.1%; Score 68; DB 3; Length 898;
Best Local Similarity 77.8%; Pred. No. 0.05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
 | | | | | | : | | | | | |
Db 372 LFLLLLALGLIYCRKKEG 389

RESULT 5

US-09-014-969-13

; Sequence 13, Application US/09014969

; Patent No. 5965397

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/014,969

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-014-969-13

Query Match 60.5%; Score 52; DB 2; Length 408;
Best Local Similarity 56.2%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKK 16
::|:|| |:| |||:
Db 32 ILLVLLCLLLYYCRRK 47

RESULT 6

US-09-248-796A-23224

; Sequence 23224, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23224
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-23224

Query Match 55.8%; Score 48; DB 4; Length 66;
Best Local Similarity 53.8%; Pred. No. 2.9;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYC 13
:::|:|||:
Db 33 VLILILILILIYC 45

RESULT 7

US-09-198-452A-1162
; Sequence 1162, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1162
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1162

Query Match 54.7%; Score 47; DB 4; Length 91;
Best Local Similarity 47.1%; Pred. No. 5.7;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17
| ::|||::: || :|
Db 69 LSLIVLVLLIIECRNRE 85

RESULT 8
US-09-438-185A-175
; Sequence 175, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0173
US-09-438-185A-175

Query Match 54.7%; Score 47; DB 4; Length 109;
Best Local Similarity 47.1%; Pred. No. 6.9;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17
| |::|||::: || :|
Db 87 LSLIVLVLLIIECRNRE 103

RESULT 9

US-08-123-161A-10

; Sequence 10, Application US/08123161A

; Patent No. 5449616

; GENERAL INFORMATION:

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Roberds, Steven L.

; APPLICANT: Anderson, Richard D.

; APPLICANT: Ibraghimov, Oxana B.

; APPLICANT: Yang, Bin

; TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999

; CITY: York Harbor

; STATE: ME

; COUNTRY: USA

; ZIP: 03911

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123,161A

; FILING DATE: 16-SEP-93

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/946,234

; FILING DATE: 14-SEP-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Farrell, Kevin M.

; REGISTRATION NUMBER: 35,505

; REFERENCE/DOCKET NUMBER: UIRF89-11A4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (207) 363-0558

; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-161A-10

Query Match 53.5%; Score 46; DB 1; Length 387;

Best Local Similarity 55.0%; Pred. No. 35;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| |:| | | | :|||
Db 299 LVALLLALLAYIMCCRREG 318

RESULT 10

US-08-123-161A-12

; Sequence 12, Application US/08123161A

; Patent No. 5449616

; GENERAL INFORMATION:

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Roberds, Steven L.

; APPLICANT: Anderson, Richard D.

; APPLICANT: Ibraghimov, Oxana B.

; APPLICANT: Yang, Bin

; TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999

; CITY: York Harbor

; STATE: ME

; COUNTRY: USA

; ZIP: 03911

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123,161A

; FILING DATE: 16-SEP-93

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/946,234

; FILING DATE: 14-SEP-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Farrell, Kevin M.

; REGISTRATION NUMBER: 35,505

; REFERENCE/DOCKET NUMBER: UIRF89-11A4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (207) 363-0558

; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-161A-12

Query Match 53.5%; Score 46; DB 1; Length 387;
Best Local Similarity 55.0%; Pred. No. 35;

Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| :| | | ::||
Db 299 LVALLTLLAYVMCCRREG 318

RESULT 11

US-08-483-278-10

; Sequence 10, Application US/08483278

; Patent No. 5686073

; GENERAL INFORMATION:

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Ibraghimov, Oxana B.

; APPLICANT: Ervasti, James M.

; APPLICANT: Leveille, Cynthia J.

; TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999

; CITY: York Harbor

; STATE: ME

; COUNTRY: USA

; ZIP: 03911

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,278

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/123,161

; FILING DATE: 16-SEP-93

; ATTORNEY/AGENT INFORMATION:

; NAME: Farrell, Kevin M.

; REGISTRATION NUMBER: 35,505

; REFERENCE/DOCKET NUMBER: UIRF89-11A5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (207) 363-0558

; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-483-278-10

Query Match 53.5%; Score 46; DB 1; Length 387;

Best Local Similarity 55.0%; Pred. No. 35;

Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| |:| | | :|||
DB 299 LVALLLALLAYIMCCRREG 318

RESULT 12
US-08-483-278-12
; Sequence 12, Application US/08483278
; Patent No. 5686073
; GENERAL INFORMATION:
; APPLICANT: Campbell, Kevin P.
; APPLICANT: Ibraghimov, Oxana B.
; APPLICANT: Ervasti, James M.
; APPLICANT: Leveille, Cynthia J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,278
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,161
; FILING DATE: 16-SEP-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: UIRF89-11A5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-278-12

Query Match 53.5%; Score 46; DB 1; Length 387;
Best Local Similarity 55.0%; Pred. No. 35;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| |:| | | :|||

Db 299 LVALLTLLAYVMCCRREG 318

RESULT 13
US-09-949-016-9728
; Sequence 9728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9728
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9728

Query Match 53.5%; Score 46; DB 4; Length 392;
Best Local Similarity 55.0%; Pred. No. 35;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| |:| | | :||
Db 304 LVALLTLLAYVMCCRREG 323

RESULT 14
US-09-489-039A-10360
; Sequence 10360, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10360
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10360

Query Match 52.3%; Score 45; DB 4; Length 483;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
|:||| ||| ::| : |
Db 31 LLLLLFVLIALWCHGRPG 48

RESULT 15

US-10-101-464A-932

; Sequence 932, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell
Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 932
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-932

Query Match 52.3%; Score 45; DB 4; Length 635;
Best Local Similarity 53.3%; Pred. No. 80;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LLLLVLILVYCRKKE 17
|:||.||| ::|::|:
Db 269 LVLLFLILFFCKRKK 283

Search completed: March 1, 2005, 09:05:52
Job time : 1.07853 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 0.702678 Seconds
(without alignments)
2464.715 Million cell updates/sec

Title: US-10-624-932-2_COPY_372_389

Perfect score: 86

Sequence: 1 LVLLLLVLILVYCRKKEG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	56	65.1	245	2	C64616 hypothetical prote
2	53	61.6	95	2	E82696 hypothetical prote
3	48.5	56.4	1197	2	T30581 neural cell adhesi
4	48.5	56.4	1232	2	T43027 neural cell adhesi
5	47	54.7	91	2	E86512 hypothetical prote
6	47	54.7	91	2	D72109 hypothetical prote
7	47	54.7	664	2	T10573 probable serine/th
8	47	54.7	664	2	B85122 serine/threonine k
9	46	53.5	334	2	D71625 rifin PFB0015c - m
10	46	53.5	387	2	A49498 dystrophin-associa
11	46	53.5	387	2	A54746 adhalin precursor
12	46	53.5	387	2	I48201 adhalin - golden h
13	46	53.5	387	2	JC5556 adhalin - mouse

14	46	53.5	409	2	T32082	hypothetical prote
15	46	53.5	584	2	T25059	hypothetical prote
16	46	53.5	594	2	I49127	intracellular prot
17	46	53.5	828	1	T00534	S-receptor kinase
18	45	52.3	133	2	T30474	hypothetical prote
19	45	52.3	276	2	S20690	31.6K hypothetical
20	45	52.3	304	2	A83928	sugar transport sy
21	45	52.3	312	2	E71624	rifin PFB0055c - m
22	45	52.3	314	2	T16300	hypothetical prote
23	45	52.3	893	2	A47550	bride of sevenless
24	45	52.3	896	2	S26740	gene boss protein
25	45	52.3	896	2	A36455	bride of sevenless
26	45	52.3	1143	2	T10636	hypothetical prote
27	44	51.2	71	2	B83730	hypothetical prote
28	44	51.2	168	2	E69119	conserved hypothet
29	44	51.2	171	2	S09903	hypothetical prote
30	44	51.2	171	2	S09759	hypothetical prote
31	44	51.2	197	2	F70385	conserved hypothet
32	44	51.2	234	2	S28999	G protein-coupled
33	44	51.2	273	2	B86504	CT016 hypothetical
34	44	51.2	273	2	A72120	conserved hypothet
35	44	51.2	309	2	I49522	gene B7-2 protein
36	44	51.2	330	2	D71600	rifin PFB1035w - m
37	44	51.2	356	2	F71624	rifin PFB0060w - m
38	44	51.2	357	2	T34012	hypothetical prote
39	44	51.2	386	2	D71851	tetracycline resis
40	44	51.2	444	2	F81367	probable transmemb
41	44	51.2	540	2	G96716	hypothetical prote
42	44	51.2	551	2	S64314	probable membrane
43	44	51.2	588	2	I37202	B-CAM protein - hu
44	44	51.2	628	2	I38000	Lutheran blood gro
45	44	51.2	680	2	JC8052	protein tyrosine p

ALIGNMENTS

RESULT 1

C64616

hypothetical protein HP0771 - *Helicobacter pylori* (strain 26695)

C;Species: *Helicobacter pylori*

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: C64616

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: C64616

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-245 <TOM>
A;Cross-references: UNIPROT:O25463; GB:AE000589; GB:AE000511; NID:g2313895;
PIDN:AAD07824.1; PID:g2313903; TIGR:HP0771

Query Match 65.1%; Score 56; DB 2; Length 245;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
 | :||:||:||::|:
Db 167 LALILLILVLIYCKRLFG 184

RESULT 2
E82696
hypothetical protein XF1308 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82696
R;anonymous, The Xylella fastidiosa Consortium of the Organization for
Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82696
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <SIM>
A;Cross-references: UNIPROT:Q9PDS1; GB:AE003964; GB:AE003849; NID:g9106300;
PIDN:AAF84117.1; GSPDB:GN00128; XFSC:XF1308
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.;
Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros,
M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.;
Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Colauto, N.B.;
Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.;
Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.;
Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco,
M.C.; Frohme, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.;
Gomes, S.L.; Gruber, A.; Ho, P.L.; Hoheisel, J.D.; Junqueira, M.L.; Kemper,
E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.;
Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado,
J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques,
M.V.; Martins, E.A.L.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.;
Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento,
A.L.T.O.; Netto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira,
M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto,
B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.;
Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.;
Santelli, R.V.; Sawasaki, H.E.

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza, A.P.; Terenzi, M.F.; Truffi, D.; Tsai, S.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zatz, M.; Meidanis, J.; Setubal, J.C.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF1308

Query Match 61.6%; Score 53; DB 2; Length 95;
Best Local Similarity 55.6%; Pred. No. 2.6;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
Db :|::|: |: | |||||
74 VVIVLVFLLTVDCKKEG 91

RESULT 3

T30581

neural cell adhesion molecule L1.1 - zebra fish (fragment)

C;Species: Brachydanio rerio (zebra fish)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30581

R;Tongiorgi, E.; Bernhardt, R.R.; Schachner, M.

J. Neurosci. Res. 42, 547-561, 1995

A;Title: Zebrafish neurons express two L1-related molecules during early axonogenesis.

A;Reference number: Z20875; MUID:96155762; PMID:8568941

A;Accession: T30581

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1197 <TON>

A;Cross-references: UNIPROT:Q90478; EMBL:X89204; NID:g1065713; PID:g1065714; PIDN:CAA61490.1

C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; immunoglobulin homology

Query Match 56.4%; Score 48.5; DB 2; Length 1197;
Best Local Similarity 63.2%; Pred. No. 55;
Matches 12; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 LVLLLLVLILV-YCRKKEG 18
Db |||||||:|: | :| :|
1062 LVLLLLVLLLLCYIKKSKG 1080

RESULT 4

T43027

neural cell adhesion molecule L1 - goldfish

N;Alternate names: E587 antigen

C;Species: Carassius auratus (goldfish)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43027

R;Giordano, S.; Laessing, U.; Lottspeich, F.; Stuermer, C.A.O.

submitted to the EMBL Data Library, April 1996

A;Description: Molecular cloning of goldfish E587 antigen, a cell adhesion molecule expressed in the CNS.
A;Reference number: Z22294
A;Accession: T43027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1232 <GIO>
A;Cross-references: UNIPROT:Q90284; EMBL:U55211; NID:g1305526; PID:g1305527;
PIDN:AAA99159.1
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: cell adhesion; membrane protein

Query Match 56.4%; Score 48.5; DB 2; Length 1232;
Best Local Similarity 68.4%; Pred. No. 56;
Matches 13; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 LVLLLLV-LILVYCRKKEG 18
| | | | | | || | : | : |
Db 1098 LVLLLLVLLILCYIKKSKG 1116

RESULT 5
E86512
hypothetical protein CPj0173 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86512
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.;
Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T.
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86512
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>
A;Cross-references: UNIPROT:Q9Z911; GB:BA000008; NID:g8978546; PIDN:BAA98383.1;
GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0173

Query Match 54.7%; Score 47; DB 2; Length 91;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17
| | :: | | :: | | : |
Db 69 LSLIVLVLLIIECRNRE 85

RESULT 6
D72109
hypothetical protein CP0597 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: D72109; D81558
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.;
Grimwood, J.; Davis, R.W.; Stephens, R.S.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: D72109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <ARN>
A;Cross-references: UNIPROT:Q9Z911; GB:AE001604; GB:AE001363; NID:g4376438;
PIDN:AAD18326.1; PID:g4376442
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
C.M.
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: D81558
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <REA>
A;Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38414.1;
PID:g7189510; GSPDB:GN00122; TIGR:CP0597
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0173; CP0597

Query Match 54.7%; Score 47; DB 2; Length 91;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17
| |::|||::: || :|
Db 69 LSLIVLVLLIIECRNRE 85

RESULT 7
T10573
probable serine/threonine-specific protein kinase (EC 2.7.1.-) F25E4.150 -
Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2004
C;Accession: T10573
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell,
B.G.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueler, C.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: T10573
A;Molecule type: DNA
A;Residues: 1-664 <BEV>
A;Cross-references: UNIPROT:Q9LDQ3; EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.150

A;Experimental source: cultivar Columbia; BAC clone F25E4

C;Genetics:

A;Gene: ATSP:F25E4.150

A;Map position: 4

A;Note: intron positions not resolved

C;Superfamily: protein kinase homology

C;Keywords: phosphotransferase; protein kinase

Query Match 54.7%; Score 47; DB 2; Length 664;
Best Local Similarity 47.1%; Pred. No. 58;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17

::|: ||::|| ||::|:

Db 291 VILVSLVVLLVVCRRKK 307

RESULT 8

B85122

serine/threonine kinase-like protein (partial) [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004

C;Accession: B85122

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The
Cold Spring Harbor, Washington University in St Louis and PE Biosystems
Arabidopsis Sequencing Consortium.

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85122

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-664 <STOP>

A;Cross-references: UNIPROT:Q9LDQ3; GB:NC_001268; NID:g7267853; PIDN:CAB78196.1;
GSPDB:GN00140

C;Genetics:

A;Gene: AT4g11530

A;Map position: 4

C;Superfamily: protein kinase homology

Query Match 54.7%; Score 47; DB 2; Length 664;
Best Local Similarity 47.1%; Pred. No. 58;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17

::|: ||::|| ||::|:

Db 291 VILVSLVVLLVVCRRKK 307

RESULT 9

D71625

rifin PFB0015c - malaria parasite (*Plasmodium falciparum*)

C;Species: Plasmodium falciparum

C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C;Accession: D71625

R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Shallom, S.; Mason, T.; Yu, K.; Fujii, C.; Pederson, J.; Shen, K.; Jing, J.; Aston, C.; Lai, Z.; Schwartz, D.C.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Fraser, C.M.; Adams, M.D.; Venter, J.C.; Hoffman, S.L.

Science 282, 1126-1132, 1998

A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A;Reference number: A71600; MUID:99021743; PMID:9804551

A;Accession: D71625

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-334 <GAR>

A;Cross-references: UNIPROT:O96109; GB:AE001366; GB:AE001362; NID:g3845070;

PIDN:AACT1793.1; PID:g3845072; TIGR:PFB0015c

A;Experimental source: clone 3D7

C;Genetics:

A;Gene: PFB0015c

C;Superfamily: Plasmodium falciparum rifin PFB1005w

Query Match 53.5%; Score 46; DB 2; Length 334;
Best Local Similarity 58.8%; Pred. No. 49;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17

||:|:: ||| | |||:

Db 305 LVMLIIYLILRYRRKKK 321

RESULT 10

A49498

dystrophin-associated glycoprotein 50k - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C;Accession: A49498

R;Roberds, S.L.; Anderson, R.D.; Ibraghimov-Beskrovnaya, O.; Campbell, K.P. J. Biol. Chem. 268, 23739-23742, 1993

A;Title: Primary structure and muscle-specific expression of the 50-kDa dystrophin-associated glycoprotein (Adhalin).

A;Reference number: A49498; MUID:94043181; PMID:8226900

A;Accession: A49498

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-387 <ROB>

A;Cross-references: GB:U01117

C;Genetics:

A;Gene: DAG2

C;Superfamily: mouse adhalin

C;Keywords: glycoprotein

Query Match 53.5%; Score 46; DB 2; Length 387;
Best Local Similarity 55.0%; Pred. No. 55;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18

|| ||| |:| | | :||

Db 299 LVALLLALLAYIMCCRREG 318

RESULT 11

A54746

adhalin precursor - human

C;Species: Homo sapiens (man)

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C;Accession: A54746; I39405

R;Roberds, S.L.; Leturcq, F.; Allamand, V.; Piccolo, F.; Jeanpierre, M.; Anderson, R.D.; Lim, L.E.; Lee, J.C.; Tome, F.M.S.; Romero, N.B.; Fardeau, M.; Beckmann, J.S.; Kaplan, J.C.; Campbell, K.P.

Cell 78, 625-633, 1994

A;Title: Missense mutations in the adhalin gene linked to autosomal recessive muscular dystrophy.

A;Reference number: A54746; MUID:94349366; PMID:8069911

A;Accession: A54746

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-387 <ROB>

A;Cross-references: UNIPROT:Q16586; GB:U08895; NID:g511586; PIDN:AAA81637.1; PID:g511587

R;Passos-Bueno, M.R.; Moreira, E.S.; Vainzof, M.; Chamberlain, J.S.; Marie, S.K.; Pereira, L.V.; Akiyama, J.; Roberds, S.L.; Campbell, K.P.; Zatz, M. Hum. Mol. Genet. 4, 1163-1167, 1995

A;Title: A common missense mutation in the adhalin gene in three unrelated Brazilian families with a relatively mild form of autosomal recessive limb-girdle muscular dystrophy.

A;Reference number: I39405; MUID:96133290; PMID:8528203

A;Accession: I39405

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-76, 'C', 78-214 <RES>

A;Cross-references: GB:L46810; NID:g950328; PIDN: AAC37583.1; PID:g950329

C;Superfamily: mouse adhalin

Query Match 53.5%; Score 46; DB 2; Length 387;
Best Local Similarity 55.0%; Pred. No. 55;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| |:| | | | ::||

Db 299 LVALLLALLAYIMCCRREG 318

RESULT 12

I48201

adhalin - golden hamster

C;Species: Mesocricetus auratus (golden hamster)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I48201

R;Roberds, S.L.; Campbell, K.P.

FEBS Lett. 364, 245-249, 1995

A;Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.

A;Reference number: I48201; MUID:95278335; PMID:7758576

A;Accession: I48201

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: UNIPROT:Q64255; EMBL:U21677; NID:g726481; PIDN:AAA81645.1;
PID:g726482
C;Superfamily: mouse adhalin

Query Match 53.5%; Score 46; DB 2; Length 387;
Best Local Similarity 55.0%; Pred. No. 55;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| :| | | :||
Db 299 LVALLLTLLAYIMCCRREG 318

RESULT 13
JC5556
adhalin - mouse
N;Alternate names: alpha-sarcoglycan
C;Species: Mus musculus (house mouse)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5556
R;Liu, L.; Vachon, P.H.; Kuang, W.; Xu, H.; Wewer, U.M.; Kylsten, P.; Engvall, E.
Biochem. Biophys. Res. Commun. 235, 227-235, 1997
A;Title: Mouse adhalin: Primary structure and expression during late stages of muscle differentiation in vitro.
A;Reference number: JC5556; MUID:97339469; PMID:9196068
A;Accession: JC5556
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-387 <LIU>
A;Cross-references: UNIPROT:P82350; GB:AF019564; NID:g2411509; PIDN:AAB70754.1;
PID:g2411510
C;Comment: This protein is a component of the sarcoglycan complex in muscle membranes. It is specific for striated muscle and it is linked with the formation of a fully functional muscle fiber.
C;Superfamily: mouse adhalin

Query Match 53.5%; Score 46; DB 2; Length 387;
Best Local Similarity 55.0%; Pred. No. 55;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVY--CRKKEG 18
|| ||| :| | | :||
Db 299 LVALLLTLLAYIMCFRREG 318

RESULT 14
T32082
hypothetical protein T07D3.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32082
R;Lamar, B.; Wamsley, P.; Twyman, B.
submitted to the EMBL Data Library, July 1997

A;Description: The sequence of C. elegans cosmid T07D3.
A;Reference number: Z21121
A;Accession: T32082
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <LAM>
A;Cross-references: UNIPROT:O16723; EMBL:AF016682; PIDN:AAB66184.1;
GSPDB:GN00020; CESP:T07D3.4
A;Experimental source: strain Bristol N2; clone T07D3
C;Genetics:
A;Gene: CESP:T07D3.4
A;Map position: 2
A;Introns: 3/2; 56/3; 98/3; 141/2; 183/3; 266/3; 309/1; 345/3

Query Match 53.5%; Score 46; DB 2; Length 409;
Best Local Similarity 62.5%; Pred. No. 57;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKK 16
| ||:||||| | :|
Db 14 LFLLILVLILYICSRK 29

RESULT 15
T25059
hypothetical protein T21B6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25059
R;Cottage, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19975
A;Accession: T25059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-584 <WIL>
A;Cross-references: UNIPROT:Q22629; EMBL:Z68011; PIDN:CAA92012.1; GSPDB:GN00028;
CESP:T21B6.1
A;Experimental source: clone T21B6
C;Genetics:
A;Gene: CESP:T21B6.1
A;Map position: X
A;Introns: 73/3; 113/3; 253/2; 544/3

Query Match 53.5%; Score 46; DB 2; Length 584;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 10; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

Qy 1 LVLLLLVLILVYCR--KKEG 18
|:||: | |::|| | | |
Db 481 LLLLIAVAAIIYCACIKKSG 500

Search completed: March 1, 2005, 09:07:21
Job time : 1.70268 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 3.46437 Seconds
(without alignments)
1704.439 Million cell updates/sec

Title: US-10-624-932-2_COPY_372_389

Perfect score: 86

Sequence: 1 LVLLLLVLILVYCRKKEG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	100.0	130	15	US-10-296-115-966	Sequence 966, App
2	86	100.0	544	10	US-09-970-944-14	Sequence 14, Appl
3	86	100.0	557	10	US-09-933-261-6	Sequence 6, Appl
4	86	100.0	557	14	US-10-256-702-6	Sequence 6, Appl
5	86	100.0	842	15	US-10-311-623-1	Sequence 1, Appl
6	86	100.0	898	10	US-09-918-779-2	Sequence 2, Appl
7	86	100.0	898	15	US-10-624-932-2	Sequence 2, Appl
8	86	100.0	899	10	US-09-970-944-2	Sequence 2, Appl
9	68	79.1	898	10	US-09-933-261-5	Sequence 5, Appl
10	68	79.1	898	10	US-09-970-944-13	Sequence 13, Appl
11	68	79.1	898	14	US-10-256-702-5	Sequence 5, Appl
12	68	79.1	898	14	US-10-240-154-16	Sequence 16, Appl
13	56	65.1	245	9	US-09-895-913A-48	Sequence 48, Appl
14	53	61.6	826	16	US-10-033-388-2	Sequence 2, Appl
15	52	60.5	326	16	US-10-437-963-151783	Sequence 151783,
16	52	60.5	675	16	US-10-437-963-143077	Sequence 143077,
17	52	60.5	892	16	US-10-408-765A-654	Sequence 654, App
18	52	60.5	947	16	US-10-437-963-151784	Sequence 151784,
19	50.5	58.7	653	16	US-10-437-963-123872	Sequence 123872,
20	47	54.7	91	15	US-10-289-762-1162	Sequence 1162, Ap
21	47	54.7	637	16	US-10-437-963-170248	Sequence 170248,
22	46	53.5	69	15	US-10-424-599-215366	Sequence 215366,
23	46	53.5	278	15	US-10-424-599-267766	Sequence 267766,
24	45	52.3	79	16	US-10-437-963-108909	Sequence 108909,
25	45	52.3	90	15	US-10-424-599-153147	Sequence 153147,
26	45	52.3	167	10	US-09-796-753-140	Sequence 140, App
27	45	52.3	448	16	US-10-767-701-44476	Sequence 44476, A
28	45	52.3	531	15	US-10-403-571-158	Sequence 158, App
29	45	52.3	635	14	US-10-101-464A-932	Sequence 932, App
30	44.5	51.7	467	14	US-10-191-398A-4	Sequence 4, Appl
31	44.5	51.7	467	14	US-10-044-897-4	Sequence 4, Appl
32	44.5	51.7	467	14	US-10-044-901-4	Sequence 4, Appl
33	44.5	51.7	468	9	US-09-860-232A-8	Sequence 8, Appl
34	44	51.2	192	15	US-10-264-049-3892	Sequence 3892, Ap
35	44	51.2	214	9	US-09-782-980-23	Sequence 23, Appl
36	44	51.2	214	15	US-10-303-502-2	Sequence 2, Appl
37	44	51.2	214	16	US-10-806-018-23	Sequence 23, Appl
38	44	51.2	255	15	US-10-289-762-123	Sequence 123, App
39	44	51.2	276	15	US-10-335-977-5848	Sequence 5848, Ap
40	44	51.2	303	10	US-09-441-411-15	Sequence 15, Appl
41	44	51.2	303	10	US-09-441-411-20	Sequence 20, Appl
42	44	51.2	309	9	US-09-425-762-23	Sequence 23, Appl
43	44	51.2	309	9	US-09-837-867A-21	Sequence 21, Appl
44	44	51.2	309	10	US-09-441-411-13	Sequence 13, Appl
45	44	51.2	309	10	US-09-441-411-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
 US-10-296-115-966
 ; Sequence 966, Application US/10296115
 ; Publication No. US20040053248A1

; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 966
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-966

Query Match 100.0%; Score 86; DB 15; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
||| ||| ||| ||| |||
Db 42 LVLLLLVLILVYCRKKEG 59

RESULT 2
US-09-970-944-14
; Sequence 14, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-944-14

Query Match 100.0%; Score 86; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
||| ||| ||| ||| |||
Db 18 LVLLLLVLILVYCRKKEG 35

RESULT 3

US-09-933-261-6

; Sequence 6, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030040046A1 Relevant
; TOPOLOGY: No. US20030040046A1 Relevant

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-933-261-6

Query Match 100.0%; Score 86; DB 10; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |

Db 30 LVLLLLVLILVYCRKKEG 47

RESULT 4
US-10-256-702-6
; Sequence 6, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030059859A1 Relevant
; TOPOLOGY: No. US20030059859A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-256-702-6

Query Match 100.0%; Score 86; DB 14; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18

|||||||||||||||
Db 30 LVLLLLVLILVYCRKKEG 47

RESULT 5
US-10-311-623-1
; Sequence 1, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Danniel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CD1
US-10-311-623-1

Query Match 100.0%; Score 86; DB 15; Length 842;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
|||||||||||||||
Db 316 LVLLLLVLILVYCRKKEG 333

RESULT 6
US-09-918-779-2
; Sequence 2, Application US/09918779

; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-918-779-2

Query Match 100.0%; Score 86; DB 10; Length 898;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | | | | | | | | | | | | | | |
Db 372 LVLLLLVLILVYCRKKEG 389

RESULT 7

US-10-624-932-2

; Sequence 2, Application US/10624932
; Publication No. US20040096877A1

; GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US

; CURRENT APPLICATION NUMBER: US/10/624,932

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: 09/918,779

; PRIOR FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/221,409

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 60/222,840

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,752

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,762

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,770

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,769

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/225,146

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/225,392

; PRIOR FILING DATE: 2000-08-15

; PRIOR APPLICATION NUMBER: 60/225,470

; PRIOR FILING DATE: 2000-08-15

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 898

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-624-932-2

Query Match 100.0%; Score 86; DB 15; Length 898;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18

||||||||||||||||||

Db 372 LVLLLLVLILVYCRKKEG 389

RESULT 8

US-09-970-944-2

; Sequence 2, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 899

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-970-944-2

Query Match 100.0%; Score 86; DB 10; Length 899;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18

||||||||||||||||||

Db 373 LVLLLLVLILVYCRKKEG 390

RESULT 9

US-09-933-261-5

; Sequence 5, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030040046A1 Relevant
; TOPOLOGY: No. US20030040046A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-933-261-5

Query Match 79.1%; Score 68; DB 10; Length 898;
Best Local Similarity 77.8%; Pred. No. 0.6;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| .||| | |:|||||||
Db 372 LFLLLALGLIYCRKKEG 389

RESULT 10
US-09-970-944-13
; Sequence 13, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-970-944-13

Query Match 79.1%; Score 68; DB 10; Length 898;
Best Local Similarity 77.8%; Pred. No. 0.6;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| | || | | :| | | | | |
Db 372 LFLLLLALGLIYCRKKEG 389

RESULT 11
US-10-256-702-5
; Sequence 5, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030059859A1 Relevant
; TOPOLOGY: No. US20030059859A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-256-702-5

Query Match 79.1%; Score 68; DB 14; Length 898;
Best Local Similarity 77.8%; Pred. No. 0.6;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| |||| | |:|||||||
Db 372 LFLLLLALGLIYCRKKEG 389

RESULT 12

US-10-240-154-16

; Sequence 16, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-240-154-16

Query Match 79.1%; Score 68; DB 14; Length 898;
Best Local Similarity 77.8%; Pred. No. 0.6;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| |||| | |:|||||||
Db 372 LFLLLLALGLIYCRKKEG 389

RESULT 13
US-09-895-913A-48
; Sequence 48, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides
in the Helicobacter
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-48

Query Match 65.1%; Score 56; DB 9; Length 245;
Best Local Similarity 50.0%; Pred. No. 7.3;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVLLLLVLILVYCRKKEG 18
| :||:||:||:||:|
Db 167 LALILLILVLIYCKRLFG 184

RESULT 14
US-10-033-388-2
; Sequence 2, Application US/10033388
; Publication No. US20040180398A1
; GENERAL INFORMATION:
; APPLICANT: Paul O. Sheppard
; APPLICANT: Si Lok
; TITLE OF INVENTION: Mammalian Secretory Protein Zsig43
; FILE REFERENCE: 98-15C1
; CURRENT APPLICATION NUMBER: US/10/033,388
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/109,915
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: 09/440,484
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-033-388-2

Query Match 61.6%; Score 53; DB 16; Length 826;
Best Local Similarity 56.2%; Pred. No. 56;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKK 16
|||:|| |:: |||:
Db 328 LVLILLCLLIYYCRRR 343

RESULT 15

US-10-437-963-151783

; Sequence 151783, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 151783

; LENGTH: 326

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(326)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_51896C.1.pep

US-10-437-963-151783

Query Match 60.5%; Score 52; DB 16; Length 326;
Best Local Similarity 64.7%; Pred. No. 32;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VLLLLVLILVYCRKKEG 18
|:|||||||: | | |
Db 19 VVILLVLILVWLRLNKNG 35

Search completed: March 1, 2005, 09:51:31
Job time : 4.46437 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 3.29278 Seconds
(without alignments)
2799.282 Million cell updates/sec

Title: US-10-624-932-2_COPY_372_389

Perfect score: 86

Sequence: 1 LVLLLLVLILVYCRKKEG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	100.0	842	1	UN5A_HUMAN	Q6zn44 homo sapien
2	83	96.5	898	1	UN5A_MOUSE	Q8kls4 mus musculu
3	68	79.1	898	1	UN5A_RAT	O08721 rattus norv
4	58	67.4	1173	2	Q84WF4	Q84wf4 arabidopsis
5	58	67.4	1173	2	Q9FL28	Q9fl28 arabidopsis
6	56	65.1	245	2	O25463	O25463 helicobacte
7	56	65.1	529	2	Q8A1W3	Q8a1w3 bacteroides
8	53	61.6	95	2	Q9PDS1	Q9pds1 xylella fas
9	53	61.6	638	2	Q6P2L1	Q6p2l1 mus musculu
10	52	60.5	675	2	Q8H811	Q8h811 oryza sativ
11	52	60.5	892	2	Q9Y438	Q9y438 homo sapien
12	50.5	58.7	638	2	Q75GM0	Q75gm0 oryza sativ
13	50	58.1	254	2	Q72UR1	Q72url leptospira
14	50	58.1	267	2	Q8F085	Q8f085 leptospira
15	49.5	57.6	387	2	Q9RG52	Q9rg52 legionella

16	49	57.0	137	2	O96335	O96335 brugia mala
17	49	57.0	421	2	Q9E200	Q9e200 cercopithec
18	48.5	56.4	1197	1	CAM1_BRARE	Q90478 brachydanio
19	48.5	56.4	1232	2	Q90284	Q90284 carassius a
20	48.5	56.4	1269	2	Q6U7I5	Q6u7i5 brachydanio
21	48	55.8	524	2	Q8IFN8	Q8ifn8 plasmodium
22	48	55.8	775	2	Q8XNT7	Q8xnt7 clostridium
23	47.5	55.2	699	2	Q8MY74	Q8my74 ptychodera
24	47	54.7	91	2	Q9Z911	Q9z911 chlamydia p
25	47	54.7	270	2	Q9D8G2	Q9d8g2 mus musculu
26	47	54.7	370	2	Q7TSN7	Q7tsn7 mus musculu
27	47	54.7	487	2	Q65FG2	Q65fg2 bacillus li
28	47	54.7	628	2	Q9MZ08	Q9mz08 bos taurus
29	47	54.7	664	2	Q9LDQ3	Q9ldq3 arabidopsis
30	47	54.7	780	2	Q7EZB0	Q7ezb0 oryza sativ
31	47	54.7	872	2	Q26045	Q26045 proliferati
32	47	54.7	961	2	Q7WUA4	Q7wua4 porphyromon
33	47	54.7	1016	2	Q90ZF2	Q90zf2 xenopus lae
34	47	54.7	1050	2	Q6AX49	Q6ax49 xenopus lae
35	46.5	54.1	220	2	Q8ERG9	Q8erg9 oceanobacil
36	46.5	54.1	1383	2	Q7Q840	Q7q840 anopheles g
37	46	53.5	73	2	Q7JJ37	Q7jj37 felis silve
38	46	53.5	233	2	Q68PJ0	Q68pj0 vasdavidius
39	46	53.5	245	2	Q8GQD0	Q8gqd0 leptospira
40	46	53.5	245	2	Q72WC8	Q72wc8 leptospira
41	46	53.5	245	2	Q8FA27	Q8fa27 leptospira
42	46	53.5	306	2	Q8I4P2	Q8i4p2 plasmodium
43	46	53.5	334	2	O96109	O96109 plasmodium
44	46	53.5	334	2	O97724	O97724 felis silve
45	46	53.5	337	2	Q9U6Q4	Q9u6q4 plasmodium

ALIGNMENTS

RESULT 1

UN5A_HUMAN

ID UN5A_HUMAN STANDARD; PRT; 842 AA.
 AC Q6ZN44; Q8TF26; Q96GP4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
 GN Name=UNC5A; Synonyms=KIAA1976, UNC5H1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togoya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 302-842 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 624-728 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21842142; PubMed=11853319;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXII.
The complete sequences of 50 new cDNA clones which code for large

RT proteins.";
RL DNA Res. 8:319-327(2001).
RN [4]
RP INDUCTION.
RX PubMed=12598906; DOI=10.1038/ncb943;
RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
RT "p53RDL1 regulates of p53-dependent apoptosis.";
RL Nat. Cell Biol. 5:216-223(2003).
RN [5]
RP DOWN-REGULATION IN CANCER.
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
RT "The netrin-1 receptors UNC5H are putative tumor suppressors
controlling cell death commitment.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with MAGED1. Interacts with PRKCABP, possibly mediating some
CC interaction with PKC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
CC with PRKCABP regulates its surface expression and leads to its
CC removal from surface of neurons and growth cones (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q6ZN44-1; Sequence=Displayed;
CC Note>No experimental confirmation available;
CC Name=2;
CC IsoId=Q6ZN44-2; Sequence=VSP_011694, VSP_011695;
CC Note>No experimental confirmation available;
CC Name=3;
CC IsoId=Q6ZN44-3; Sequence=VSP_011693;
CC Note>No experimental confirmation available;
CC -!- INDUCTION: By p53/TP53.
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
CC participates in the induction of apoptosis (By similarity).
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues.
CC Phosphorylated by PKC in vitro (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
CC cancers.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC -!- SIMILARITY: Contains 1 ZU5 domain.

CC -!- CAUTION: Ref.3 sequence differs from that shown due to the
 CC presence of introns.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AK131380; BAD18531.1; -.
 DR EMBL; BC009333; AAH09333.2; -.
 DR EMBL; BC033727; -; NOT_ANNOTATED_CDS.
 DR EMBL; AB075856; BAB85562.1; ALT_SEQ.
 DR Genew; HGNC:12567; UNC5A.
 DR MIM; 607869; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 1.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 842 Netrin receptor UNC5A.
 FT DOMAIN 1 306 Extracellular (Potential).
 FT TRANSMEM 307 327 Potential.
 FT DOMAIN 328 842 Cytoplasmic (Potential).
 FT DOMAIN 44 141 Ig-like.
 FT DOMAIN 155 234 Ig-like C2-type.
 FT DOMAIN 242 294 TSP type-1.
 FT DOMAIN 439 542 ZU5.
 FT DOMAIN 761 841 Death..
 FT SITE 340 341 Cleavage (by caspase-3) (By similarity).
 FT SITE 605 623 Interaction with DCC (By similarity).
 FT DISULFID 65 124 By similarity.
 FT DISULFID 170 221 By similarity.
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 287 287 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 1 97 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPD
 FT LLPHFLVEPEDVYIVKKNKPVLLVCKAVPATQIFFKCNGEWV
 FT RQVDHVIERSTDGSN -> MAGTSERSLSISSIONPKAIIECF
 FT EVKKKAFLTHGRYHGSGATPPPDKDPKPETFCGQT (in
 FT isoform 3).
 FT /FTId=VSP_011693.
 FT VARSPLIC 296 301 TASGPE -> SESSLP (in isoform 2).
 FT /FTId=VSP_011694.
 FT VARSPLIC 302 842 Missing (in isoform 2).
 FT /FTId=VSP_011695.

SQ SEQUENCE 842 AA; 92958 MW; 3DFADCF973131849 CRC64;
 Query Match 100.0%; Score 86; DB 1; Length 842;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVLLLLVLILVYCRKKEG 18
 |||||||
 Db 316 LVLLLLVLILVYCRKKEG 333

RESULT 2

UN5A_MOUSE

ID UN5A_MOUSE STANDARD; PRT; 898 AA.
 AC Q8K1S4; Q6PEF7; Q80T71;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
 GN Name=Unc5a; Synonyms=Kiaa1976, Unc5h1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Brain;
 RX MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
 RA Nakajima D., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:35-48(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand (By
CC similarity).
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with MAGED1. Interacts with PRKCABP, possibly mediating some
CC interaction with PKC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
CC with PRKCABP regulates its surface expression and leads to its
CC removal from surface of neurons and growth cones (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q8K1S4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K1S4-2; Sequence=VSP_011697;
CC Note>No experimental confirmation available;
CC Name=3;
CC IsoId=Q8K1S4-3; Sequence=VSP_011696;
CC Note>No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
CC participates in the induction of apoptosis (By similarity).
CC -!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic
CC tyrosine residues (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ487852; CAD32250.1; -.

DR EMBL; AK122575; BAC65857.1; ALT_INIT.
 DR EMBL; BC058084; AAH58084.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894682; Unc5a.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 898 Netrin receptor UNC5A.
 FT DOMAIN 26 361 Extracellular (Potential).
 FT TRANSMEM 362 382 Potential.
 FT DOMAIN 383 898 Cytoplasmic (Potential).
 FT DOMAIN 44 141 Ig-like.
 FT DOMAIN 155 234 Ig-like C2-type.
 FT DOMAIN 242 296 TSP type-1 1.
 FT DOMAIN 298 350 TSP type-1 2.
 FT DOMAIN 495 598 ZU5.
 FT DOMAIN 817 897 Death.
 FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
 FT SITE 661 679 Interaction with DCC (By similarity).
 FT DISULFID 65 124 By similarity.
 FT DISULFID 170 221 By similarity.
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 343 343 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 1 790 Missing (in isoform 3).
 FT VARSPLIC 241 296 /FTId=VSP_011696.
 FT VARSPLIC 241 296 Missing (in isoform 2).
 FT CONFLICT 217 217 /FTId=VSP_011697.
 FT CONFLICT 217 217 A -> P (in Ref. 3).
 SQ SEQUENCE 898 AA; 98856 MW; 59F04BA2E196C1DB CRC64;

 Query Match 96.5%; Score 83; DB 1; Length 898;
 Best Local Similarity 83.3%; Pred. No. 0.01;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 QY 1 LVLLLLVLILVYCRKKEG 18
 |||||||:||:|||||||

Db

372 LLLLLVLVLIYCRKKEG 389

RESULT 3

UN5A_RAT

ID UN5A_RAT STANDARD; PRT; 898 AA.
AC 008721;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=Unc5a; Synonyms=Unc5h1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
SPECIFICITY.
RC TISSUE=Ventral spinal cord;
RX MEDLINE=97271897; PubMed=9126742;
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
RA Tessier-Lavigne M.;
RT "Vertebrate homologues of *C. elegans* UNC-5 are candidate netrin
receptors.";
RL Nature 386:833-838(1997).
RN [2]
RP FUNCTION, AND INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";
RL Cell 97:927-941(1999).
RN [3]
RP TISSUE SPECIFICITY.
RX PubMed=11472849;
RA Barrett C., Guthrie S.;
RT "Expression patterns of the netrin receptor UNC5H1 among developing
RT motor neurons in the embryonic rat hindbrain.";
RL Mech. Dev. 106:163-166(2001).
RN [4]
RP FUNCTION.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).
RN [5]
RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.
RX PubMed=12598531; DOI=10.1074/jbc.M300415200;
RA Williams M.E., Strickland P., Watanabe K., Hinck L.;
RT "UNC5H1 induces apoptosis via its juxtamembrane region through an
RT interaction with NRAGE.";
RL J. Biol. Chem. 278:17483-17490(2003).
RN [6]
RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF

RP 896-ALA--CYS-898.
RX PubMed=14672991; DOI=23/36/11279;
RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;
RT "Surface expression of the netrin receptor UNC5H1 is regulated through
RT a protein kinase C-interacting protein/protein kinase-dependent
RT mechanism.";
RL J. Neurosci. 23:11279-11288 (2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with MAGED1. Interacts with PRKCABP, possibly mediating some
CC interaction with PKC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
CC with PRKCABP regulates its surface expression and leads to its
CC removal from surface of neurons and growth cones.
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Expressed at early stages of neural tube development in
CC the ventral spinal cord. In developing hindbrain, it colocalizes
CC with a number of cranial motor neuron subpopulations from
CC embryonic E11 to E14, while DCC is expressed by motor neurons at
CC E12. Also expressed in non-neural structures, such as the basal
CC plane of the hindbrain and midbrain, in the developing
CC hypothalamus, thalamus and in the pallidum.
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
CC participates in the induction of apoptosis.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity). Phosphorylated by PKC in vitro.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC -----
DR EMBL; U87305; AAB57678.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621755; Unc5h1.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PRO1705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 898 Netrin receptor UNC5A.
 FT DOMAIN 26 361 Extracellular (Potential).
 FT TRANSMEM 362 382 Potential.
 FT DOMAIN 383 898 Cytoplasmic (Potential).
 FT DOMAIN 44 141 Ig-like.
 FT DOMAIN 155 238 Ig-like C2-type.
 FT DOMAIN 242 296 TSP type-1 1.
 FT DOMAIN 298 350 TSP type-1 2.
 FT DOMAIN 495 598 ZU5.
 FT DOMAIN 817 897 Death.
 FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
 FT SITE 661 679 Interaction with DCC (By similarity).
 FT DISULFID 65 124 By similarity.
 FT DISULFID 170 221 By similarity.
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 343 343 N-linked (GlcNAc. . .) (Potential).
 FT MUTAGEN 896 898 Missing: Abolishes interaction with PRKCABP.
 SQ SEQUENCE 898 AA; 98840 MW; 7A3CBCB9E7ACA135 CRC64;

 Query Match 79.18; Score 68; DB 1; Length 898;
 Best Local Similarity 77.8%; Pred. No. 0.9;
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 LVLLLLVLILVYCRKKEG 18
 | ||||| | :|||||||
 Db 372 LFLLLLALGLIYCRKKEG 389

RESULT 4
 Q84WF4
 ID Q84WF4 PRELIMINARY; PRT; 1173 AA.
 AC Q84WF4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative leucine-rich repeat transmembrane protein kinase.
 GN Name=At5g46330;

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BT003880; AAO41929.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00560; LRR_1; 27.
DR PRINTS; PR00019; LEURICRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
KW Transmembrane.
SQ SEQUENCE 1173 AA; 128823 MW; 6AFC909E48339359 CRC64;

Query Match 67.4%; Score 58; DB 2; Length 1173;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVLLLLVLILVYCRKKE 17
|:::|||||| |:|||
Db 819 LLVLLLVLIITCCKKKE 835

RESULT 5
Q9FL28
ID Q9FL28 PRELIMINARY; PRT; 1173 AA.
AC Q9FL28;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Receptor protein kinase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
CC --!- SIMILARITY: Belongs to the Ser/Thr-protein kinase family.
DR EMBL; AB010698; BAB11088.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00560; LRR_1; 27.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 1173 AA; 128823 MW; 6AF93B467A339359 CRC64;

Query Match 67.4%; Score 58; DB 2; Length 1173;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKE 17
|:::||||||| |:|||
Db 819 LLVLLLVLILTCCKKKE 835

RESULT 6
O25463
ID O25463 PRELIMINARY; PRT; 245 AA.
AC O25463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0771.
GN OrderedLocusNames=HP0771;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000589; AAD07824.1; -.
DR PIR; C64616; C64616.
DR TIGR; HP0771; -.
KW Complete proteome.
SQ SEQUENCE 245 AA; 28695 MW; AFE7F93D17AC63EA CRC64;

Query Match 65.1%; Score 56; DB 2; Length 245;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKKEG 18
| |:||:||:||:: |
Db 167 LALILLILVLIYCKRLFG 184

RESULT 7

Q8A1W3
ID Q8A1W3 PRELIMINARY; PRT; 529 AA.
AC Q8A1W3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BT3545;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016941; AAO78651.1; -.
DR InterPro; IPR008940; Prenyl_trans.
DR InterPro; IPR007016; Wzy_C.
DR Pfam; PF04932; Wzy_C; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 529 AA; 61134 MW; 00ADEBA6697A2226 CRC64;

Query Match 65.1%; Score 56; DB 2; Length 529;
Best Local Similarity 62.5%; Pred. No. 22;

Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKK 16
||||||:|::|| :|
Db 273 LVLLLLMVIIIYCYRK 288

RESULT 8

Q9PDS1

ID Q9PDS1 PRELIMINARY; PRT; 95 AA.
AC Q9PDS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf1308;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovskii-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003964; AAF84117.1; -.
DR PIR; E82696; E82696.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 95 AA; 10508 MW; 9B3E04AC7FFE550B CRC64;

Query Match 61.6%; Score 53; DB 2; Length 95;
 Best Local Similarity 55.6%; Pred. No. 17;
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

 QY 1 LVLLLLVLILVYCRKKEG 18
 ::::|: |: | |||||
 Db 74 VVIVLVFLLTVDCRKKEG 91

RESULT 9

Q6P2L1

ID Q6P2L1 PRELIMINARY; PRT; 638 AA.
 AC Q6P2L1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CDNA sequence BC025575.
 GN Name=BC025575;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC064455; AAH64455.1; -.
 SQ SEQUENCE 638 AA; 67806 MW; 369EEDE6EA6CD54E CRC64;

Query Match 61.6%; Score 53; DB 2; Length 638;
 Best Local Similarity 56.2%; Pred. No. 61;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVLLLLVLILVYCRKK 16
| ||:|| |:: |||:
Db 144 LVLILLCLLIYYCRRR 159

RESULT 10

Q8H811

ID Q8H811 PRELIMINARY; PRT; 675 AA.
AC Q8H811;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative leucine-rich repeat transmembrane protein kinase.
GN Name=OJ1743A09.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC105364; AAN05336.1; -.
DR Gramene; Q8H811; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00560; LRR_1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transmembrane.
SQ SEQUENCE 675 AA; 70751 MW; 0A42A39C0B0B1601 CRC64;

Query Match 60.5%; Score 52; DB 2; Length 675;
Best Local Similarity 73.3%; Pred. No. 85;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VLLLLVLILVYCRKK 16
||||| || : ||||
Db 278 VLLLLALIFLLCRKK 292

RESULT 11

Q9Y438

ID Q9Y438 PRELIMINARY; PRT; 892 AA.
AC Q9Y438;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp564A026 (Fragment).
 GN Name=DKFZp564A026;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL050367; CAB43675.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 892 AA; 97822 MW; ODD1730EAD604C4B CRC64;

 Query Match 60.5%; Score 52; DB 2; Length 892;
 Best Local Similarity 56.2%; Pred. No. 1e+02;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 LVLLLLVLILVYCRKK 16
 ::|:|| |:| |||:
 Db 318 ILLVLLCLLYYCRRK 333

RESULT 12
 Q75GM0
 ID Q75GM0 PRELIMINARY; PRT; 638 AA.
 AC Q75GM0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative phytosulfokine receptor kinase.
 GN Name=OSJNBa0018K15.19;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
 RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
 RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC144737; AAT01376.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.

DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR003591; LRR_typ.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00560; LRR_1; 5.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00369; LRR_TYP; 3.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Receptor.
 SQ SEQUENCE 638 AA; 69908 MW; 40E59E4F8841C6EF CRC64;

 Query Match 58.7%; Score 50.5; DB 2; Length 638;
 Best Local Similarity 47.6%; Pred. No. 1.3e+02;
 Matches 10; Conservative 7; Mismatches 1; Indels 3; Gaps 1;

 Qy 1 LVLLLLVLILVYC--RKKEG 18
 |:||:|::|:|: || |||:
 Db 267 LLLLILIVVLLICIFKRKKDG 287

RESULT 13
 Q72UR1
 ID Q72UR1 PRELIMINARY; PRT; 254 AA.
 AC Q72UR1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative lipoprotein..
 GN OrderedLocusNames=LIC10596;
 OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni).
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=44275;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fiocruz L1-130;
 RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
 RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
 RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
 RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
 RA Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,
 RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
 RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
 RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
 RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
 RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
 RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
 RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
 RT "Comparative genomics of two Leptospira interrogans serovars reveals
 novel insights into physiology and pathogenesis.";
 RL J. Bacteriol. 186:2164-2172(2004).

DR EMBL; AE017289; AAS69217.1; -.
 DR InterPro; IPR008940; Prenyl_trans.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF00515; TPR_1; 2.
 DR SMART; SM00028; TPR; 3.
 DR PROSITE; PS50005; TPR; 1.
 DR PROSITE; PS50293; TPR_REGION; 1.
 KW Complete proteome; Repeat; TPR repeat.
 SQ SEQUENCE 254 AA; 29316 MW; CCA253D17C3F0D2D CRC64;

 Query Match 58.1%; Score 50; DB 2; Length 254;
 Best Local Similarity 58.8%; Pred. No. 79;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

 Qy 1 LVLLLLVLILVYCRKKE 17
 |: :|||| :| | |||
 Db 8 LIAILLVLSIVNCNKKE 24

 RESULT 14
 Q8F085
 ID Q8F085 PRELIMINARY; PRT; 267 AA.
 AC Q8F085;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE TPR-repeat-containing proteins.
 GN OrderedLocusNames=LA3611;
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
 Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
 Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 interrogans revealed by whole-genome sequencing.";
 RL Nature 422:888-893(2003).
 DR EMBL; AE011516; AAN50809.1; -.
 DR InterPro; IPR008940; Prenyl_trans.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF00515; TPR_1; 2.
 DR SMART; SM00028; TPR; 3.
 DR PROSITE; PS50005; TPR; 1.
 DR PROSITE; PS50293; TPR_REGION; 1.
 KW Complete proteome; Repeat; TPR repeat.
 SQ SEQUENCE 267 AA; 30915 MW; 8BE13CA8BC5BA0A9 CRC64;

 Query Match 58.1%; Score 50; DB 2; Length 267;
 Best Local Similarity 58.8%; Pred. No. 82;

Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 LVLLLLVLILVYCRKKE 17
|: :||| :| | |||
Db 21 LIAILLVLSIVNCNKKE 37

RESULT 15

Q9RG52

ID Q9RG52 PRELIMINARY; PRT; 387 AA.
AC Q9RG52;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transport protein.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AA100;
RX MEDLINE=20072707; PubMed=10603410;
RX DOI=10.1128/IAI.68.12.6970-6978.2000;
RA Harb O.S., Abu Kwaik Y.;
RT "Characterization of a macrophage-specific infectivity locus (mila) of
RT Legionella pneumophila.";
RL Infect. Immun. 68:368-376(2000).
DR EMBL; AF153695; AAD47247.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
SQ SEQUENCE 387 AA; 42793 MW; 03E577FBEDA08FAE CRC64;

Query Match 57.6%; Score 49.5; DB 2; Length 387;
Best Local Similarity 55.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 1 LVLLLLVLILV---YCRKKE 17
|:| || |:|: ||| |||
Db 365 LILALLTLLLIDETYCRTKE 384

Search completed: March 1, 2005, 09:03:39
Job time : 5.29278 secs